



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/786,926A

Source: \_\_\_\_\_

Date Processed by STIC: 1/6/03  
10/10/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003



IFW16

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/786,926A

DATE: 10/10/2003  
 TIME: 10:55:39

Input Set : A:\pto.yf.txt  
 Output Set : N:\CRF4\10102003\I786926A.raw

3 <110> APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin  
 5 <120> TITLE OF INVENTION: Human and murine G-protein coupled EDG6 receptor  
 6 (endothelial differentiation gene) and use of same  
 8 <130> FILE REFERENCE: 101195-45  
 9  
 10 <140> CURRENT APPLICATION NUMBER: US/09/786,926A  
 11 <141> CURRENT FILING DATE: 2001-05-04  
 13 <150> PRIOR APPLICATION NUMBER: DE 198 43 240.2  
 14 <151> PRIOR FILING DATE: 1998-09-11  
 16 <150> PRIOR APPLICATION NUMBER: DE 198 46 979.9  
 17 <151> PRIOR FILING DATE: 1998-10-13  
 19 <150> PRIOR APPLICATION NUMBER: PCT/DE 99/02871  
 20 <151> PRIOR FILING DATE: 1999-09-10  
 E--> 22 <160> NUMBER OF SEQ ID NOS: 416(p.3)  
 24 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

263 <210> SEQ ID NO: 5  
 264 <211> LENGTH: 30  
 265 <212> TYPE: DNA  
 266 <213> ORGANISM: Artificial Sequence  
 W--> 267 <220> FEATURE:  
 268 <223> OTHER INFORMATION: Sequence of PCR Primer R1  
 270 <400> SEQUENCE: 5  
 E--> 272 cgg gat cgg cvt dvt sgg maa ykb vyt sgt  
 275 <210> SEQ ID NO: 6  
 276 <211> LENGTH: 29  
 277 <212> TYPE: DNA  
 278 <213> ORGANISM: Artificial Sequence  
 W--> 279 <220> FEATURE:  
 280 <223> OTHER INFORMATION: Sequence of PCR Primer R3  
 282 <400> SEQUENCE: 6  
 E--> 284 cgg gat cgg aar gyr tas ads adr ggr tt  
 287 <210> SEQ ID NO: 7  
 288 <211> LENGTH: 21  
 289 <212> TYPE: DNA  
 290 <213> ORGANISM: Artificial Sequence  
 W--> 291 <220> FEATURE:  
 292 <223> OTHER INFORMATION: Sequence of PCR Primer 5'hGSPRT  
 294 <400> SEQUENCE: 7  
 E--> 296 ttg gag cca aag acg tgg gcc  
 298 <210> SEQ ID NO: 8

Does Not Comply  
 Corrected Diskette Needed

pp 1-3

30< insert cumulative  
 nucleotide total at right  
 margin of each line

29< insert

21<

## RAW SEQUENCE LISTING

DATE: 10/10/2003

PATENT APPLICATION: US/09/786,926A

TIME: 10:55:39

Input Set : A:\pto.yf.txt

Output Set: N:\CRF4\10102003\I786926A.raw

```

299 <211> LENGTH: 21
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
W--> 302 <220> FEATURE:
303 <223> OTHER INFORMATION: Sequence of PCR Primer 5'hGSP1
305 <400> SEQUENCE: 8
E--> 307 agg cag aag agg atg tag cgc 21<
310 <210> SEQ ID NO: 9
311 <211> LENGTH: 21
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
W--> 314 <220> FEATURE:
315 <223> OTHER INFORMATION: Sequence of PCR Primer 5'hGSP2
317 <400> SEQUENCE: 9
E--> 319 ggc ctc ccc tgc agt gaa gag 21<
322 <210> SEQ ID NO: 10
323 <211> LENGTH: 21
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
W--> 326 <220> FEATURE:
327 <223> OTHER INFORMATION: Sequence of PCR Primer 3'hGSP1
329 <400> SEQUENCE: 10
E--> 331 agt gac ctg ctc acg ggc ggc 21<
333 <210> SEQ ID NO: 11
334 <211> LENGTH: 21
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequence
W--> 337 <220> FEATURE:
338 <223> OTHER INFORMATION: Sequence of PCR Primer 3'hGSP2
340 <400> SEQUENCE: 11
E--> 342 ctc ttc act gca ggc gag cgc 21<
345 <210> SEQ ID NO: 12
346 <211> LENGTH: 24
347 <212> TYPE: DNA
348 <213> ORGANISM: Artificial Sequence
W--> 349 <220> FEATURE:
350 <223> OTHER INFORMATION: Sequence of PCR Primer 5'mGSPRT
352 <400> SEQUENCE: 12
E--> 354 ctc acc tgc tat ggc agg gcc tgc 24<
358 <210> SEQ ID NO: 13
359 <211> LENGTH: 24
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial Sequence
W--> 362 <220> FEATURE:
363 <223> OTHER INFORMATION: Sequence of PCR Primer 5'mGSP1
365 <400> SEQUENCE: 13
E--> 367 tgg gca act ggc tgg tcc aag ctc 24<
370 <210> SEQ ID NO: 14
371 <211> LENGTH: 49

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/786,926A

DATE: 10/10/2003

TIME: 10:55:39

Input Set : A:\pto.yf.txt

Output Set: N:\CRF4\10102003\I786926A.raw

372 <212> TYPE: DNA  
 373 <213> ORGANISM: Artificial Sequence  
 375 <220> FEATURE:  
 376 <223> OTHER INFORMATION: Sequence of PCR Primer 5'mGSP2  
 378 <400> SEQUENCE: 14  
 E--> 379 gcc tog ggc oca gat cat oca ggg gtg ctg egg acg ctg gaa atg ctg g  
 383 <210> SEQ ID NO: 15  
 384 <211> LENGTH: 21  
 385 <212> TYPE: DNA  
 386 <213> ORGANISM: Artificial Sequence  
 W--> 387 <220> FEATURE:  
 388 <223> OTHER INFORMATION: Sequence of 3' primer  
 390 <400> SEQUENCE: 15  
 E--> 392 oca cgt cat cat gac agc agc 21←  
 400 <210> SEQ ID NO: 16  
 401 <211> LENGTH: 21  
 402 <212> TYPE: DNA  
 403 <213> ORGANISM: Artificial Sequence  
 W--> 404 <220> FEATURE:  
 405 <223> OTHER INFORMATION: Sequence of CA primer  
 407 <400> SEQUENCE: 16  
 E--> 409 oca cgt cat cat gac agc agc 21←  
 E--> 412

*insert a hard  
 return after nucleotide  
 at location 48. Per  
 1.822 of sequence rules,  
 a maximum  
 of 48  
 triplets  
 per line*

*last sequence in submitted file*

*delete*

## VERIFICATION SUMMARY

DATE: 10/10/2003

PATENT APPLICATION: US/09/786,926A

TIME: 10:55:40

Input Set : A:\pto.yf.txt

Output Set: N:\CRF4\10102003\I786926A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:30 M:283 W: Missing Blank Line separator, <220> field identifier  
L:119 M:283 W: Missing Blank Line separator, <220> field identifier  
L:150 M:283 W: Missing Blank Line separator, <220> field identifier  
L:181 M:283 W: Missing Blank Line separator, <220> field identifier  
L:267 M:283 W: Missing Blank Line separator, <220> field identifier  
L:272 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:5  
L:279 M:283 W: Missing Blank Line separator, <220> field identifier  
L:284 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:6  
L:291 M:283 W: Missing Blank Line separator, <220> field identifier  
L:296 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:7  
L:302 M:283 W: Missing Blank Line separator, <220> field identifier  
L:307 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:8  
L:314 M:283 W: Missing Blank Line separator, <220> field identifier  
L:319 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:9  
L:326 M:283 W: Missing Blank Line separator, <220> field identifier  
L:331 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:10  
L:337 M:283 W: Missing Blank Line separator, <220> field identifier  
L:342 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:11  
L:349 M:283 W: Missing Blank Line separator, <220> field identifier  
L:354 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:12  
L:362 M:283 W: Missing Blank Line separator, <220> field identifier  
L:367 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:13  
L:379 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:49 SEQ:14  
L:387 M:283 W: Missing Blank Line separator, <220> field identifier  
L:392 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:15  
L:404 M:283 W: Missing Blank Line separator, <220> field identifier  
L:409 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:16  
M:254 Repeated in SeqNo=16  
L:22 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (4) Counted (16)